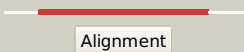

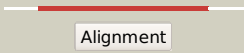



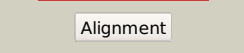



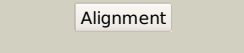

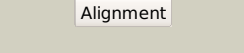



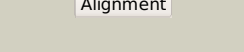

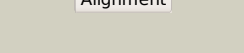

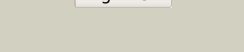



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0418_(lpqL)_503499_505001
Date	Tue Jul 23 14:50:49 BST 2019
Unique Job ID	562b28aedf883600

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4tweA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylated-alpha-linked acidic dipeptidase-like protein; PDBTitle: structure of ligand-free n-acetylated-alpha-linked-acidic-dipeptidase2 like protein (naaladasel)
2	c2ootA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
3	c1cx8F_	 Alignment		100.0	21	PDB header: metal transport Chain: F: PDB Molecule: transferrin receptor protein; PDBTitle: crystal structure of the ectodomain of human transferrin receptor
4	c3rbuA_	 Alignment		100.0	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: glutamate carboxypeptidase 2; PDBTitle: n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
5	c3iibA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m28; PDBTitle: crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
6	c2ek8A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: aminopeptidase from aneurinibacillus sp. strain am-1
7	d1tkja1	 Alignment		100.0	54	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
8	c6eslB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: bacterial leucyl aminopeptidase; PDBTitle: crystal structure of the legionella pneumoppila lapa
9	c5gneA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of lapb from legionella pneumophila
10	c4fbeA_	 Alignment		100.0	20	PDB header: transferase, hydrolase Chain: A: PDB Molecule: cg5976, isoform b; PDBTitle: crystal structure of the c136a/c164a variant of mitochondrial isoform2 of glutaminy cyclase from drosophila melanogaster
11	c4f9vB_	 Alignment		100.0	24	PDB header: transferase, hydrolase Chain: B: PDB Molecule: cg32412; PDBTitle: structure of c113a/c136a mutant variant of glycosylated glutaminy2 cyclase from drosophila melanogaster

12	c6qqkB_	Alignment		100.0	27	PDB header: transferase Chain: B; PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of porphyromonas gingivalis glutaminy cyclase
13	c3pb6X_	Alignment		100.0	28	PDB header: transferase Chain: X; PDB Molecule: glutaminy-peptide cyclotransferase-like protein; PDBTitle: crystal structure of the catalytic domain of human golgi-resident2 glutaminy cyclase at ph 6.5
14	d1de4c3	Alignment		100.0	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
15	c4mhzA_	Alignment		100.0	25	PDB header: transferase Chain: A; PDB Molecule: glutaminy cyclase, putative; PDBTitle: crystal structure of apo-form glutaminy cyclase from ixodes2 scapularis in complex with pbd150
16	d1rtqa_	Alignment		100.0	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
17	c3tc8A_	Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a zn-dependent exopeptidase (bdj_3547) from2 parabacteroides distasonis atcc 8503 at 1.06 a resolution
18	d2afwa1	Alignment		100.0	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminy-peptide cyclotransferase-like
19	c4fuuA_	Alignment		100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: leucine aminopeptidase; PDBTitle: crystal structure of a leucine aminopeptidase precursor (bt_2548) from2 bacteroides thetaiotaomicron vpi-5482 at 1.30 a resolution
20	d3bi1a3	Alignment		100.0	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
21	c4r12A_	Alignment	not modelled	100.0	13	PDB header: protein binding Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the gamma-secretase component nicastrin
22	c3guxA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: putative zn-dependent exopeptidase; PDBTitle: crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
23	c5a63A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: nicastrin; PDBTitle: cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
24	c3k9tA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
25	c4uisA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex
26	d1vhoo2	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
27	c4upcA_	Alignment	not modelled	100.0	19	PDB header: protein binding Chain: A; PDB Molecule: nicastrin; PDBTitle: structure of a extracellular domain
28	d1xfoa2	Alignment	not modelled	99.9	25	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases

29	d1yloa2	Alignment	not modelled	99.9	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
30	d1z2la1	Alignment	not modelled	99.9	25	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
31	d1vhea2	Alignment	not modelled	99.9	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
32	d2fvga2	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
33	d1cg2a1	Alignment	not modelled	99.9	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
34	d1fnoa4	Alignment	not modelled	99.8	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
35	d1r3na1	Alignment	not modelled	99.8	30	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
36	d1lfwa1	Alignment	not modelled	99.8	18	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
37	d1vixa1	Alignment	not modelled	99.8	18	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
38	d3bi1a2	Alignment	not modelled	99.8	18	Fold: The "swivelling" beta/beta/alpha domain Superfamily: PA domain Family: PA domain
39	d1de4c2	Alignment	not modelled	99.7	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: PA domain Family: PA domain
40	c3t6mA	Alignment	not modelled	99.7	24	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of dape protein from <i>Vibrio cholerae</i> in the Zn-bound form
41	c2pokB	Alignment	not modelled	99.4	27	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of a m20 family metallo peptidase from <i>Streptococcus pneumoniae</i>
42	c3icuA	Alignment	not modelled	99.4	20	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rnf128; PDBTitle: protease-associated domain of the e3 ligase graII
43	c4tjvA	Alignment	not modelled	99.3	22	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting receptor 1; PDBTitle: crystal structure of protease-associated domain of <i>Arabidopsis thaliana</i> vacuolar sorting receptor 1
44	c5i4mB	Alignment	not modelled	99.3	27	PDB header: hydrolase Chain: B: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of amidase, hydantoinase/carbamoylase family from <i>Burkholderia vietnamiensis</i>
45	c2greC	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: C: PDB Molecule: deblocking aminopeptidase; PDBTitle: crystal structure of deblocking aminopeptidase from <i>Bacillus cereus</i>
46	c1q7IA	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: A: PDB Molecule: aminoacylase-1; PDBTitle: Zn-binding domain of the t347g mutant of human aminoacylase-2 I
47	c1cg2D	Alignment	not modelled	99.3	23	PDB header: metallocarboxypeptidase Chain: D: PDB Molecule: carboxypeptidase g2; PDBTitle: carboxypeptidase g2
48	c2zogA	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic non-specific dipeptidase; PDBTitle: crystal structure of mouse carnosinase cn2 complexed with Zn and 2 bestatin
49	c1vhoA	Alignment	not modelled	99.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of a putative peptidase/endoglucanase
50	c4pxeB	Alignment	not modelled	99.2	25	PDB header: hydrolase Chain: B: PDB Molecule: ureidoglycolate hydrolase; PDBTitle: the crystal structure of atuah in complex with glyoxylate
51	c5k8nE	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: E: PDB Molecule: 5-nitroanthranilic acid aminohydrolase; PDBTitle: 5naa-bound 5-nitroanthranilate aminohydrolase
52	c4g1pA	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: cys-gly metallodipeptidase dug1; PDBTitle: structural and mechanistic basis of substrate recognition by novel di-2 peptidase dug1p from <i>Saccharomyces cerevisiae</i>
53	c1ysjB	Alignment	not modelled	99.2	21	PDB header: hydrolase Chain: B: PDB Molecule: protein yxep; PDBTitle: crystal structure of <i>Bacillus subtilis</i> yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
54	c4h2kA	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of the catalytic domain of succinyl-diaminopimelate2 desuccinylase from <i>Haemophilus influenzae</i>
55	c3rzaA	Alignment	not modelled	99.2	21	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidase; PDBTitle: crystal structure of a tripeptidase (sav1512) from

						staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
56	d1xmba1	Alignment	not modelled	99.2	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
57	c3gb0A	Alignment	not modelled	99.2	23	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution
58	c4ewtC	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: C: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: the crystal structure of a putative aminohydrolase from methicillin2 resistant staphylococcus aureus
59	c1vgyB	Alignment	not modelled	99.1	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of succinyl diaminopimelate desuccinylase
60	c3pfoB	Alignment	not modelled	99.1	22	PDB header: hydrolase Chain: B: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
61	c3dljB	Alignment	not modelled	99.1	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-ala-his dipeptidase; PDBTitle: crystal structure of human carnosine dipeptidase 1
62	c3khzA	Alignment	not modelled	99.1	19	PDB header: hydrolase Chain: A: PDB Molecule: putative dipeptidase sacol1801; PDBTitle: crystal structure of r350a mutant of staphylococcus aureus2 metallopeptidase (sapep/dape) in the apo-form
63	c2qyvB	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: B: PDB Molecule: xaa-his dipeptidase; PDBTitle: crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
64	d1ysja1	Alignment	not modelled	99.1	18	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
65	c3ifeA	Alignment	not modelled	99.0	28	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
66	c3kl9F	Alignment	not modelled	99.0	23	PDB header: hydrolase Chain: F: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of pepa from streptococcus pneumoniae
67	c3n5fB	Alignment	not modelled	99.0	39	PDB header: hydrolase Chain: B: PDB Molecule: n-carbamoyl-l-amino acid hydrolase; PDBTitle: crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
68	c3ic1A	Alignment	not modelled	99.0	19	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
69	c2q43A	Alignment	not modelled	99.0	23	PDB header: hydrolase Chain: A: PDB Molecule: iaa-amino acid hydrolase ilr1-like 2; PDBTitle: ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
70	d1y0ya2	Alignment	not modelled	98.9	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
71	c5tp4B	Alignment	not modelled	98.9	38	PDB header: hydrolase Chain: B: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of a hydantoinase/carbamoylase family amidase from2 burkholderia ambifaria
72	c3pfeA	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of a m20a metallo peptidase (dape, lpg0809) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution
73	c2v8gD	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: D: PDB Molecule: beta-alanine synthase; PDBTitle: crystal structure of beta-alanine synthase from2 saccharomyces kluveri in complex with the product beta-3 alanine
74	c3x3eA	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: A: PDB Molecule: n-acetyl-lysine deacetylase; PDBTitle: crystal structure of lysk from thermus thermophilus complex with2 lysine
75	c1vixA	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of a putative peptidase t
76	c1lfwA	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: pepv; PDBTitle: crystal structure of pepv
77	c6c0dA	Alignment	not modelled	98.8	28	PDB header: hydrolase Chain: A: PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of an amidase (hydantoinase/carbamoylase family)2 from burkholderia phymatum
78	c3tx8A	Alignment	not modelled	98.8	25	PDB header: hydrolase Chain: A: PDB Molecule: succinyl-diaminopimelate desuccinylase; PDBTitle: crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
79	c4wwwvA	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase from family m42; PDBTitle: aminopeptidase apdkam598 from the archaeon desulfurococcus2 kamchatkensis
80	d2grea2	Alignment	not modelled	98.7	15	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases

81	c4q7aD_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: D: PDB Molecule: n-acetyl-ornithine/n-acetyl-lysine deacetylase; PDBTitle: crystal structure of n-acetyl-ornithine/n-acetyl-lysine deacetylase2 from sphaerobacter thermophilus
82	c3mruB_	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: B: PDB Molecule: aminoacyl-histidine dipeptidase; PDBTitle: crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
83	c3ramC_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: C: PDB Molecule: hmra protein; PDBTitle: crystal structure of hmra
84	c1y0yA_	Alignment	not modelled	98.6	26	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: frv operon protein frvx; PDBTitle: crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
85	c2pe3A_	Alignment	not modelled	98.6	19	PDB header: hydrolase Chain: A: PDB Molecule: 354aa long hypothetical operon protein frv; PDBTitle: crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
86	c2rb7A_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
87	c2imoA_	Alignment	not modelled	98.5	18	PDB header: hydrolase Chain: A: PDB Molecule: allantoate amidohydrolase; PDBTitle: crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
88	c3ct9B_	Alignment	not modelled	98.4	24	PDB header: hydrolase Chain: B: PDB Molecule: acetylornithine deacetylase; PDBTitle: crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31 a resolution
89	c1vheA_	Alignment	not modelled	98.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aminopeptidase/glucanase homolog; PDBTitle: crystal structure of a aminopeptidase/glucanase homolog
90	c1yloA_	Alignment	not modelled	98.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein sf2450; PDBTitle: crystal structure of protein of unknown function (possible2 aminopeptidase) s2589 from shigella flexneri 2a str. 2457t
91	c5ds0F_	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: F: PDB Molecule: peptidase m42; PDBTitle: crystal structure of tet aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon scgc ab-539-e09
92	c2fvga_	Alignment	not modelled	98.3	18	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
93	c4mmoB_	Alignment	not modelled	98.3	12	PDB header: hydrolase Chain: B: PDB Molecule: sso-cp2 metallo-carboxypeptidase; PDBTitle: the crystal structure of a m20 family metallo-carboxypeptidase sso-cp22 from sulfolobus solfataricus
94	c3isxA_	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1050) from thermotoga maritima2 at 1.40 a resolution
95	c2cf4A_	Alignment	not modelled	98.2	20	PDB header: hydrolase Chain: A: PDB Molecule: protein ph0519; PDBTitle: pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
96	c2f7vA_	Alignment	not modelled	98.2	22	PDB header: hydrolase Chain: A: PDB Molecule: acetylitrulline deacetylase; PDBTitle: structure of acetylitrulline deacetylase complexed with2 one co
97	c4wjbB_	Alignment	not modelled	98.2	25	PDB header: hydrolase Chain: B: PDB Molecule: putative amidohydrolase/peptidase; PDBTitle: x-ray crystal structure of a putative amidohydrolase/peptidase from2 burkholderia cenocepacia
98	c3l6sA_	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate
99	c3cpxC_	Alignment	not modelled	98.0	16	PDB header: hydrolase Chain: C: PDB Molecule: aminopeptidase, m42 family; PDBTitle: crystal structure of putative m42 glutamyl aminopeptidase2 (yp_676701.1) from cytophaga hutchinsonii atcc 33406 at 2.39 a3 resolution
100	c1xf1A_	Alignment	not modelled	97.9	25	PDB header: hydrolase Chain: A: PDB Molecule: c5a peptidase; PDBTitle: structure of c5a peptidase- a key virulence factor from2 streptococcus
101	d1vgya1	Alignment	not modelled	97.7	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
102	d1y7ea2	Alignment	not modelled	97.6	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
103	c4r8fB_	Alignment	not modelled	97.6	12	PDB header: hydrolase Chain: B: PDB Molecule: vacuolar aminopeptidase 1; PDBTitle: crystal structure of yeast aminopeptidase 1 (ape1)
104	c3varA_	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of dnpep, znzn form
105	c2ijzF_	Alignment	not modelled	97.4	15	PDB header: hydrolase Chain: F: PDB Molecule: probable m18-family aminopeptidase 2; PDBTitle: crystal structure of aminopeptidase

106	c2qlfB_	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: B: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: crystal structure of aminopeptidase (m18 family) from thermotoga2 maritima
107	c1y7eA_	Alignment	not modelled	97.0	13	PDB header: hydrolase Chain: A: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
108	c2qljR_	Alignment	not modelled	96.9	13	PDB header: hydrolase Chain: R: PDB Molecule: PDBTitle: crystal structure of aminopeptidase i from clostridium2 acetobutylicum
109	c5jm6D_	Alignment	not modelled	96.9	13	PDB header: hydrolase Chain: D: PDB Molecule: aminopeptidase-like protein; PDBTitle: structure of chaetomium thermophilum mape1
110	c3io1B_	Alignment	not modelled	96.8	17	PDB header: hydrolase Chain: B: PDB Molecule: aminobenzoyl-glutamate utilization protein; PDBTitle: crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
111	c4emeB_	Alignment	not modelled	96.6	20	PDB header: hydrolase Chain: B: PDB Molecule: m18 aspartyl aminopeptidase; PDBTitle: x-ray crystal structure and specificity of the plasmodium falciparum2 malaria aminopeptidase
112	c5xyrA_	Alignment	not modelled	94.8	21	PDB header: lyase Chain: A: PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species
113	c1q7lB_	Alignment	not modelled	94.0	14	PDB header: hydrolase Chain: B: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human aminoacylase-2 i
114	c4c9vA_	Alignment	not modelled	79.1	23	PDB header: signaling protein Chain: A: PDB Molecule: rnf43; PDBTitle: xenopus rnf43 ectodomain in complex with xenopus rspo2 fu1-fu2
115	c4c84B_	Alignment	not modelled	73.8	28	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase znr3; PDBTitle: zebrafish znr3 ectodomain crystal form i
116	c3i74B_	Alignment	not modelled	65.5	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: subtilisin-like protease; PDBTitle: crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
117	c3vtaB_	Alignment	not modelled	60.4	13	PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l
118	c4kngF_	Alignment	not modelled	60.0	22	PDB header: signaling protein, membrane protein Chain: F: PDB Molecule: e3 ubiquitin-protein ligase rnf43; PDBTitle: crystal structure of human lgr5-rspo1-rnf43
119	c4zebA_	Alignment	not modelled	46.8	7	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (agrocinopines a) PDBTitle: pbp acca from a. tumefaciens c58 in complex with agrocinopine a
120	d1qnaa1	Alignment	not modelled	44.4	11	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain